

SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Falco, S. Carl
Famodu, Layo O.
Hitz, William D.
Rendina, Alan

<120> Chorismate Biosynthesis Enzymes

<130> BB-1159-C

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<150> 60/093,611

<151> July 21, 1998

<160> 28

<170> Microsoft Office 97

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<212> DNA

<213> Zea mays

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 <213> Zea mays

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 Tyr Arg Pro Lys Trp Glu Gly Gly Glu Tyr Glu Gly Asp Asp Asp Ser
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 Arg Phe Glu Ala Leu Leu Leu Ala Met Glu Leu Gly Ala Glu Tyr Val
 65 70 75 80
 Asp Val Glu Leu Lys Val Ala Asp Lys Phe Met Lys Leu Ile Ser Gly
 85 90 95
 Arg Asn Pro Asp Asn Cys Lys Leu Ile Val Ser Ser His Asn Tyr Glu
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 165 170 175
 Arg Val Leu Cys Pro Lys Tyr Gly Gly Phe Leu Thr Phe Gly Ser Leu
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 Leu Val Asp Asp Leu Ala Lys Phe Leu Asp Thr Tyr Ser Ser Pro Asp
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 Tyr Val Gly Ala Ile Ser Ala Ile Glu Asp Gly Ile Lys Ala Ser Glu
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 Thr Ala Ile Gly Met His Pro Asn Val Asn Glu Thr Pro Leu Ser Lys
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 <211> 1803
 <212> DNA
 <213> Oryza sativa

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<211> 402
<212> PRT
<213> Oryza sativa

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35 40 45
Ser Asp Ile Ala Asp Val Ser Arg Met Phe Gln Val Met Val His Cys
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Gln Val Pro Met Ile Gly Leu Val Met Gly Glu Lys Gly Leu Met Ser
65 70 75 80
Arg Val Leu Ser Pro Lys Phe Gly Gly Tyr Leu Thr Phe Gly Thr Leu
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Asp Ala Thr Lys Ile Ser Ala Pro Gly Gln Pro Thr Val Lys Glu Leu
100 105 110
Leu Asp Ile Tyr Asn Ile Arg Arg Ile Gly Pro Asp Thr Lys Val Leu
115 120 125
Gly Leu Ile Ala Asn Pro Val Lys Gln Ser Lys Ser Pro Ile Leu His
130 135 140
Asn Lys Cys Leu Gln Ser Ile Gly Tyr Asn Ala Val Tyr Leu Pro Leu
145 150 155 160
Leu Ala Asp Asp Leu Ala Arg Phe Leu Ser Thr Tyr Ser Ser Pro Asp
165 170 175
Phe Ser Gly Phe Ser Cys Ser Leu Pro Phe Lys Val Asp Ala Val Gln
180 185 190
Cys Cys His Glu His Asp Pro Val Ala Lys Ser Ile Gly Ala Ile Asn
195 200 205
Thr Ile Ile Arg Arg Pro Asp Gly Lys Leu Val Gly Tyr Asn Thr Asp
210 215 220

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Tyr Ile Gly Ala Ile Ser Ala Ile Glu Asp Gly Ile Gly Gly Pro Gly
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 Ser Lys Asp Ala Ala Ile Ser Pro Leu Ala Gly Arg Leu Val Val Val
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 Val Gly Ala Gly Gly Ala Gly Lys Ala Ile Ala Tyr Gly Ala Lys Glu
 260 265 270
 Lys Gly Ala Arg Val Val Val Ala Asn Arg Thr Tyr Glu Lys Ala Val
 275 280 285
 Ser Leu Ala Ala Ala Val Gly Gly His Ala Leu Arg Leu Ala Glu Leu
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 Glu Thr Phe Arg Pro Glu Glu Gly Met Ile Leu Ala Asn Ala Thr Ser
 305 310 315 320
 Leu Gly Met Tyr Pro Asn Val Asp Gly Thr Pro Ile Pro Lys Lys Ala
 325 330 335
 Leu Ser Phe Tyr Asp Val Val Phe Asp Ala Val Tyr Ala Pro Lys Val
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 Thr Arg Leu Leu Arg Glu Ala Glu Glu Cys Gly Ile Lys Val Val Ser
 355 360 365
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 <211> 1815
 <212> DNA
 <213> Glycine max

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<212> PRT
<213> Glycine max

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Asp Val Asp Lys Ala Lys Ala Gly Gly Ala Asp Leu Val Glu Ile Arg
          35          40          45

Leu Asp Ser Leu Lys Thr Phe Asp Pro Tyr Arg Asp Leu Asn Ala Phe
          50          55          60

Ile Gln His Arg Ser Leu Pro Leu Leu Phe Thr Tyr Arg Pro Lys Trp
          65          70          75          80

Glu Gly Gly Met Tyr Asp Gly Asp Glu Asn Lys Arg Leu Asp Ala Leu
          85          90          95

Arg Leu Ala Met Glu Leu Gly Ala Asp Tyr Ile Asp Ile Glu Leu Gln
          100          105          110

Val Ala His Glu Phe Tyr Asp Ser Ile Arg Gly Lys Thr Phe Asn Lys
          115          120          125

Thr Lys Val Ile Val Ser Ser His Asn Tyr Gln Leu Thr Pro Ser Ile
          130          135          140

Glu Asp Leu Gly Asn Leu Val Ala Arg Ile Gln Ala Thr Gly Ala Asp
          145          150          155          160

Ile Val Lys Ile Ala Thr Thr Ala Leu Asp Ile Thr Asp Val Ala Arg
          165          170          175

Met Phe Gln Ile Met Val His Ser Gln Val Pro Phe Ile Gly Leu Val
          180          185          190

Met Gly Asp Arg Gly Leu Ile Ser Arg Ile Leu Ser Ala Lys Phe Gly
          195          200          205

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 Gly Gln Pro Thr Leu Lys Asp Leu Leu Tyr Leu Tyr Asn Leu Arg Gln
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 Leu Ala Pro Asp Thr Lys Val Phe Gly Ile Ile Gly Lys Pro Val Gly
 245 250 255
 His Ser Lys Ser Pro Ile Leu Phe Asn Glu Val Phe Lys Ser Ile Gly
 260 265 270
 Leu Asn Gly Val Tyr Leu Phe Leu Leu Val Asp Asp Leu Ala Asn Phe
 275 280 285
 Leu Arg Thr Tyr Ser Ser Thr Asp Phe Val Gly Phe Ser Val Thr Ile
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 Ala Lys Ser Ile Gly Ala Val Asn Cys Ile Val Arg Arg Pro Thr Asp
 325 330 335
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 340 345 350
 Ile Glu Asn Gly Leu Arg Gly Lys His Asn Gly Ser Ser Thr Thr Ile
 355 360 365
 Ser Pro Leu Ala Gly Lys Leu Phe Val Val Ile Gly Ala Gly Gly Ala
 370 375 380
 Gly Lys Ala Leu Ala Tyr Gly Ala Lys Ala Lys Gly Ala Arg Val Val
 385 390 395 400
 Ile Ala Asn Arg Thr Tyr Asp His Ala Arg Lys Leu Ala Tyr Ala Ile
 405 410 415
 Gly Gly Asp Ala Leu Ala Leu Ala Asp Leu Asp Asn Tyr His Pro Glu
 420 425 430
 Asp Gly Met Ile Leu Ala Asn Thr Thr Ser Ile Gly Met Gln Pro Lys
 435 440 445
 Val Asp Glu Thr Pro Val Ser Lys His Ala Leu Lys Tyr Tyr Ser Leu
 450 455 460
 Val Phe Asp Ala Val Tyr Thr Pro Lys Ile Thr Arg Leu Leu Lys Glu
 465 470 475 480
 Ala Glu Glu Ser Gly Ala Thr Ile Val Thr Gly Leu Glu Met Phe Met
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 <211> 539
 <212> DNA
 <213> Triticum aestivum

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 <211> 176
 <212> PRT
 <213> Triticum aestivum

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 35 40 45
 Arg Gln Ile Gly Pro Asp Thr Lys Val Phe Gly Ile Ile Gly Asn Pro
 50 55 60
 Val Gly His Ser Lys Ser Pro Ile Leu His Asn Glu Ala Phe Arg Ser
 65 70 75 80
 Val Gly Leu Asn Ala Val Tyr Val Pro Phe Leu Val Asp Asp Leu Ala
 85 90 95
 Lys Phe Leu Ser Thr Tyr Ser Ser Pro Asp Phe Ala Gly Phe Ser Cys
 100 105 110
 Thr Ile Pro His Lys Glu Ala Ala Val Arg Cys Cys Asp Glu Val Asp
 115 120 125
 Pro Ile Ala Arg Asp Ile Gly Ala Val Asn Thr Ile Ile Arg Lys Pro
 130 135 140
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 165 170 175

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 <211> 1200
 <212> DNA
 <213> Zea mays


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<210> 10
<211> 305
<212> PRT
<213> Zea mays

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Leu Arg Val Ala Asp Pro Ala Gly Pro Ala Val Ala Val Arg Ala Arg
      35          40          45

Gly Ser Lys Pro Val Ala Pro Leu Arg Leu Arg Ala Lys Lys Ser Ser
      50          55          60

Gly Gly His Glu Asn Ser His Asn Ser Val Asp Glu Ala Leu Leu Leu
      65          70          75          80

Lys Arg Lys Ser Glu Glu Val Leu Phe Tyr Leu Asn Gly Arg Cys Ile
      85          90          95

Tyr Leu Val Gly Met Met Gly Ser Gly Lys Ser Thr Val Gly Lys Ile
      100          105          110

Met Ser Glu Val Leu Gly Tyr Ser Phe Phe Asp Ser Asp Lys Leu Val
      115          120          125

Glu Gln Ala Val Gly Met Pro Ser Val Ala Gln Ile Phe Lys Val His
      130          135          140

Ser Glu Ala Phe Phe Arg Asp Asn Glu Ser Ser Val Leu Arg Asp Leu
      145          150          155          160

Ser Ser Met Arg Arg Leu Val Val Ala Thr Gly Gly Gly Ala Val Ile
      165          170          175

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Arg Pro Ile Asn Trp Arg Tyr Met Lys Arg Gly Leu Ser Val Trp Leu
180 185 190

Asp Val Pro Leu Asp Ala Leu Ala Arg Arg Ile Ala Lys Val Gly Thr
195 200 205

Ala Ser Arg Pro Leu Leu Asp Gln Pro Ser Gly Asp Pro Tyr Ala Met
210 215 220

Ala Phe Ser Lys Leu Ser Met Leu Ala Gln Gln Arg Gly Asp Ala Tyr
225 230 235 240

Ala Asn Ala Asp Val Arg Val Ser Leu Glu Glu Ile Ala Cys Lys Gln
245 250 255

Gly His Asp Asp Val Ser Lys Leu Thr Pro Thr Asp Ile Ala Ile Glu
260 265 270

Ser Leu His Lys Ile Glu Ser Phe Val Ile Glu His Thr Ala Asp Ser
275 280 285

Ser Ala Ser Asp Ala Gln Ala Glu Ser Gln Ile Gln Arg Ile Gln Thr
290 295 300

Leu
305

<210> 11
<211> 899
<212> DNA
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ggatctgtca tcaatgcata gggttggtgt tgcaaccgga ggtggtgcag tgatccgacc 360
aatcaattgg agttacatga agaaagggct gaccgtatgg ttagatgtcc cactggatgc 420
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cggatgatcct tatgcaaagg cttatgcaaa acttacgtca ctttttgagc aaagaatgga 540
ctcgtatgct aatgctgatg ccagagtttc acttgaacat attgcattaa aacaaggcca 600
taatgatgtc actatactta cacctagtag catcgccatt gaggcattgc taaagatgga 660
aagttttctt accgagaaga ccatggtcag aaactgacct cttgaatgag agggaaagga 720
tgctgacaac atgtggccct tgtttgttta attgtacata tacctttgca ttattgccta 780
aactctttct acagtgttgt tggattattg tttgtgcagc atgaaagagg accgtttgag 840
tttgtattta tgcaaatgaa taagtaaata actttcagtt aaaaaaaaaa aaaaaaaaaa 899

<210> 12
<211> 231
<212> PRT
<213> Zea mays

<400> 12
His Glu Ala Gln Ser Ala Gly Gly Thr Gly Lys Val His Tyr Ser Ala
1 5 10 15

Asp Asp Ala Leu Ile Leu Gln Gln Lys Ala Gln Asp Val Leu Pro Tyr
 20 25 30
 Leu Asp Gly Arg Cys Val Tyr Leu Val Gly Met Met Gly Ser Gly Lys
 35 40 45
 Thr Thr Val Gly Lys Ile Leu Ser Glu Val Leu Gly Tyr Ser Phe Phe
 50 55 60
 Asp Ser Asp Lys Leu Val Glu Lys Ala Val Gly Ile Ser Ser Val Ala
 65 70 75 80
 Glu Ile Phe Gln Leu His Ser Glu Thr Phe Phe Arg Asp Asn Glu Ser
 85 90 95
 Glu Val Leu Thr Asp Leu Ser Ser Met His Arg Leu Val Val Ala Thr
 100 105 110
 Gly Gly Gly Ala Val Ile Arg Pro Ile Asn Trp Ser Tyr Met Lys Lys
 115 120 125
 Gly Leu Thr Val Trp Leu Asp Val Pro Leu Asp Ala Leu Ala Arg Arg
 130 135 140
 Ile Ala Ala Val Gly Thr Ala Ser Arg Pro Leu Leu His Gln Glu Ser
 145 150 155 160
 Gly Asp Pro Tyr Ala Lys Ala Tyr Ala Lys Leu Thr Ser Leu Phe Glu
 165 170 175
 Gln Arg Met Asp Ser Tyr Ala Asn Ala Asp Ala Arg Val Ser Leu Glu
 180 185 190
 His Ile Ala Leu Lys Gln Gly His Asn Asp Val Thr Ile Leu Thr Pro
 195 200 205
 Ser Thr Ile Ala Ile Glu Ala Leu Leu Lys Met Glu Ser Phe Leu Thr
 210 215 220
 Glu Lys Thr Met Val Arg Asn
 225 230

<210> 13
 <211> 1077
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (387)

<220>
 <221> unsure
 <222> (1036)

<220>
 <221> unsure
 <222> (1038)

<220>
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 <222> (1076)

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 caccgtctcc gcgccttccc aagctcggaa atacctctag aggaactcaa cccatccgtc 180
 gatctactta ggagaactgc ggaggccgtt ggcgatttca ggaaaacgcc aatctatatt 240
 gttggtacgg attgcacagc caagcgcaac atcgccaagc tgcttgcgaa ttccataata 300
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 cagctcacgt ccatgggtaa ccttggtactg tgctgtggag atggcgccgt tatgaactca 480
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 gcaacaaatg acatgttgaa gaacacggga acacaagcta ctacagatcc agactctttt 600
 tctcaggcga tgagcaagct ccgtcagcgg tatgatgaac tgaaagagcg ctatgggggt 660
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 gcaaaggaga tgatggaagc tgcagggaag ccattctaaa caagatacac atacacaata 840
 gttctgctcc ggcatacccta ttttctggcc agttaccaag acctccgatg cttcgctgtt 900
 caagaaaccg attgcagttg cctacggctc aaagcacaag cgcgtgaaat ctaaggaact 960
 gaatctgggt gttccactcg aatatgctta tattgtattg caagatcact tgccaaaaaa 1020
 aaaaaaaaaa aactcnangg gggggcccgg tacccaattc cccctaaaat ggagtnc 1077

<210> 14
 <211> 272
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (129)

<400> 14
 Ala Met Arg Ala Ala Thr Ala Ala Ala Thr Gly Phe Phe Ser Pro Ser
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 Thr Val Pro Pro Arg Arg Phe Ser Ser Val Thr Pro Pro Ala Ser Leu
 20 25 30
 Cys Thr Ala Arg Cys Ile Gln Arg His Arg Leu Arg Ala Phe Pro Ser
 35 40 45
 Ser Glu Ile Pro Leu Glu Glu Leu Asn Pro Ser Val Asp Leu Leu Arg
 50 55 60
 Arg Thr Ala Glu Ala Val Gly Asp Phe Arg Lys Thr Pro Ile Tyr Ile
 65 70 75 80
 Val Gly Thr Asp Cys Thr Ala Lys Arg Asn Ile Ala Lys Leu Leu Ala
 85 90 95
 Asn Ser Ile Ile Tyr Arg Tyr Leu Ser Ser Glu Glu Leu Leu Glu Asp
 100 105 110
 Val Leu Gly Gly Lys Asp Ala Leu Arg Ala Phe Lys Glu Ser Asp Glu
 115 120 125
 Xaa Gly Tyr Leu Glu Val Glu Thr Glu Gly Leu Lys Gln Leu Thr Ser
 130 135 140

Met Gly Asn Leu Val Leu Cys Cys Gly Asp Gly Ala Val Met Asn Ser
145 150 155 160

Thr Asn Leu Arg Leu Leu Lys His Gly Val Ser Ile Trp Ile Asp Val
165 170 175

Pro Leu Glu Met Ala Thr Asn Asp Met Leu Lys Asn Thr Gly Thr Gln
180 185 190

Ala Thr Thr Asp Pro Asp Ser Phe Ser Gln Ala Met Ser Lys Leu Arg
195 200 205

Gln Arg Tyr Asp Glu Leu Lys Glu Arg Tyr Gly Val Ser Asp Ile Thr
210 215 220

Val Ser Val Gln Asn Val Ala Ser Gln Arg Gly Tyr Ser Ser Ile Asp
225 230 235 240

Leu Val Thr Leu Glu Asp Met Val Leu Glu Ile Val Arg Gln Ile Glu
245 250 255

Lys Leu Ile Arg Ala Lys Glu Met Met Glu Ala Ala Gly Lys Pro Phe
260 265 270

<210> 15
<211> 544
<212> DNA
<213> Oryza sativa

<400> 15
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gggttcggcg gctccgaccg ccgccggagc gcgctctacg gcggcgaggg gcgggcgcgcg 180
atcgggagct tgaggggtcg tgagccggcg gtggcgaagg ccgctgtgtg ggctcgcggg 240
tccaagccgg tcgccccgct ccgtgccaaag aaatcgctcc gaggtcatga aacattgcat 300
aactcggttg atgaagccct cttgctaaag agaaaatcag aagaagttct cttctatttg 360
aatggacggg gtattttacct agttggaatg atgggttctg gaaaaagtac tgtgggaaag 420
atcatgtctg aagttttggg ttattcggtc tttgatagtg ataaattggg caacaagctg 480
tgggcatgcc ttcagtcgct caaattttca agggcatag tgaagccttc ctttaaggata 540
gtgg 544

<210> 16
<211> 155
<212> PRT
<213> Oryza sativa

<400> 16
Met Glu Ala Gly Val Gly Leu Ala Leu Gln Ser Arg Ala Ala Gly Phe
1 5 10 15
Gly Gly Ser Asp Arg Arg Arg Ser Ala Leu Tyr Gly Gly Glu Gly Arg
20 25 30
Ala Arg Ile Gly Ser Leu Arg Val Ala Glu Pro Ala Val Ala Lys Ala
35 40 45
Ala Val Trp Ala Arg Gly Ser Lys Pro Val Ala Pro Leu Arg Ala Lys
50 55 60

Lys Ser Ser Gly Gly His Glu Thr Leu His Asn Ser Val Asp Glu Ala
65 70 75 80

Leu Leu Leu Lys Arg Lys Ser Glu Glu Val Leu Phe Tyr Leu Asn Gly
85 90 95

Arg Cys Ile Tyr Leu Val Gly Met Met Gly Ser Gly Lys Ser Thr Val
100 105 110

Gly Lys Ile Met Ser Glu Val Leu Gly Tyr Ser Val Phe Asp Ser Asp
115 120 125

Lys Leu Val Gln Gln Ala Val Gly Met Pro Ser Val Ala Gln Ile Phe
130 135 140

Lys Gly His Ser Glu Ala Phe Leu Lys Asp Ser
145 150 155

<210> 17
<211> 1098
<212> DNA
<213> Oryza sativa

<400> 17
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agtgaatcta aagaaagttg agcaagagct gaaatggccc gacattgatg aatcttggga 120
atcccttact tctggaatca ctcagctttt gacagggatt agtggtcata ttgttggtga 180
ttccacagat ataaacgagg cagttgctaa agaaatagct gaggaattg gttaccttcc 240
agtctgcaca agtgagctgc tagaaagtgc caccgaaaag tctattgaca aatgggttggc 300
ttcggaagga gtggattcgg tagcagaagc tgaatgtgtt gtgctggaaa gccttagcag 360
ccatgttcgt acagtcgtag caactctggg gggaaagcaa ggagcagcta gcagatttga 420
taaattggcag tatcttcatg ctggatttac ggtttggttg tcggtctccg atgccagcga 480
tgaagcttct gccaaagaag aggcccgtag aagtgtgagc tcgggaaatg ttgcgtacgc 540
gaaagctgat gtagtagtga agcttggtgg atgggatccg gagtacacac gagctgttgc 600
ccagggttgc cttgtggcct tgaagcagct aacattggca gacaagaagc tagcaggtaa 660
gaagagccta tacatgaggc tgggatgccg aggggattgg cccaacatcg agcctcccgg 720
ctgggatcct gactccgacg caccacccac caacatatga ttttcatact cagtactcac 780
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aaaaaaaaaa aaaaaaaa 1098

<210> 18
<211> 252
<212> PRT
<213> Oryza sativa

<400> 18
His Glu Leu Thr Ile Lys Ser Ser Glu Thr Ile Trp Phe Ile Asp Glu
1 5 10 15

Asp Gln Leu Val Val Asn Leu Lys Lys Val Glu Gln Glu Leu Lys Trp
20 25 30

Pro Asp Ile Asp Glu Ser Trp Glu Ser Leu Thr Ser Gly Ile Thr Gln
35 40 45

tgaaagagga ccgtttgagt ttgtacttgt gcaaataaat aagtaaatag ctttcagtta 900
 ggacaaaaaa aaaaaaagcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960

<210> 20
 <211> 245
 <212> PRT
 <213> Sorghum

<400> 20
 His Glu Ala Gly Pro Ala Leu Arg Pro Ala Lys Leu Arg Val Ser Cys
 1 5 10 15
 Ser Ala Lys Ser Ala Gly Thr Gly Lys Val His Tyr Ser Thr Asp Glu
 20 25 30
 Ala Leu Ile Leu Gln Gln Lys Ala Gln Asp Val Leu Pro Tyr Leu Asp
 35 40 45
 Gly Arg Cys Val Tyr Leu Val Gly Met Met Gly Ser Gly Lys Thr Thr
 50 55 60
 Val Gly Lys Ile Leu Ala Glu Val Leu Gly Tyr Ser Phe Phe Asp Ser
 65 70 75 80
 Asp Lys Leu Val Glu Lys Ala Val Gly Ile Ser Ser Val Ala Glu Ile
 85 90 95
 Phe Gln Leu His Ser Glu Ala Phe Phe Arg Asp Asn Glu Ser Glu Val
 100 105 110
 Leu Arg Asp Leu Ser Ser Met His Arg Leu Val Val Ala Thr Gly Gly
 115 120 125
 Gly Ala Val Ile Arg Pro Ile Asn Trp Ser Tyr Met Lys Lys Gly Leu
 130 135 140
 Thr Val Trp Leu Asp Val Pro Leu Asp Ala Leu Ala Arg Arg Ile Ala
 145 150 155 160
 Ala Val Gly Thr Ala Ser Arg Pro Leu Leu His Gln Glu Ser Gly Asp
 165 170 175
 Pro Tyr Ala Lys Ala Tyr Ala Lys Leu Thr Ser Leu Phe Glu Gln Arg
 180 185 190
 Met Asp Ser Tyr Ala Asn Ala Asp Ala Arg Val Ser Leu Glu His Ile
 195 200 205
 Ala Leu Lys Gln Gly His Asn Asp Val Thr Ile Leu Thr Pro Ser Ala
 210 215 220
 Ile Ala Ile Glu Ala Leu Leu Lys Met Glu Ser Phe Leu Thr Glu Lys
 225 230 235 240
 Thr Met Val Arg Asn
 245

<210> 21
 <211> 1183

<212> DNA
 <213> Glycine max

<400> 21
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 cgcaggctca attgctcagt atcagacggc accgtttcgt cttcgcttgg tgccacggac 180
 tcgtctcttg cgggtgaagaa gaaagcagca gaggtgtctt ctgagctcaa agggacctcc 240
 atatttctgg ttggtttgaa gagctctctt aaaactagtt tggggaagct gctggctgat 300
 gcattgcggt attattattt cgacagtgat agtttggtgg aagaagctgt aggtggtgca 360
 ctggctgcaa aatcattcag agagagtgc gaaaaaggct tctatgagtc tgagactgaa 420
 gtactgaagc aattatcgtc catgggtcga ctagtggttt gtgcaggaaa tggcactggt 480
 acaagctcca ctaatctggg ctttctgaga catgggattt cattatggat tgatgtgcct 540
 ctagattttg tggccagaga tgtaattgaa gataagagtc aatttgctcc atctgaaata 600
 tctatttcag gatcataccc agaggtacag gatgaactag gtgctctgta cgataaatac 660
 agagttggat atgctacagc tgatgctatt atttcagttc aaaaagtagt ttctcggtcg 720
 ggttgtgata acttagatga aattacaaga gaagacatgg ctttgagggc tcttagggaa 780
 attgagaagt tgaccagagt aaagaagatg caggaagagg ctgcaagacc attttaacca 840
 acttggacat gctcccttcc tttaccgga atcaaattgg acaatctaaa cttttttaa 900
 tttgcaatcc ctgtgttagc ttctcaaatt tcagttttct ttttagttgt tttcctttga 960
 aatttcagtc ttcctattgt tgttgttgtt ttaagactta ctctgtacta tagtgttata 1020
 taggggagga gaaaaatact ctttctgta cctccaatac aacttttttg cttacttttt 1080
 ttttcttctt tttatcaatg attacttgat ttcttctga aaaaaaaaaa aaaaaaaaaa 1140
 aaaaaaaaaa aaaaaaaaaa tcgagggggg cccgtacaca atc 1183

<210> 22
 <211> 278
 <212> PRT
 <213> Glycine max

<400> 22
 Ala Arg Gly Leu Cys His Arg Asn Thr Pro Leu Pro Leu Leu Asn Arg
 1 5 10 15
 Pro Ser Asn Phe Leu Gln Phe Lys His Gln Asn Ser Phe Leu Lys Phe
 20 25 30
 Pro Asn Pro Asn Leu His Arg Leu Arg Arg Leu Asn Cys Ser Val Ser
 35 40 45
 Asp Gly Thr Val Ser Ser Ser Leu Gly Ala Thr Asp Ser Ser Leu Ala
 50 55 60
 Val Lys Lys Lys Ala Ala Glu Val Ser Ser Glu Leu Lys Gly Thr Ser
 65 70 75 80
 Ile Phe Leu Val Gly Leu Lys Ser Ser Leu Lys Thr Ser Leu Gly Lys
 85 90 95
 Leu Leu Ala Asp Ala Leu Arg Tyr Tyr Tyr Phe Asp Ser Asp Ser Leu
 100 105 110
 Val Glu Glu Ala Val Gly Gly Ala Leu Ala Ala Lys Ser Phe Arg Glu
 115 120 125
 Ser Asp Glu Lys Gly Phe Tyr Glu Ser Glu Thr Glu Val Leu Lys Gln
 130 135 140
 Leu Ser Ser Met Gly Arg Leu Val Val Cys Ala Gly Asn Gly Thr Val
 145 150 155 160

Thr Ser Ser Thr Asn Leu Gly Leu Leu Arg His Gly Ile Ser Leu Trp
 165 170 175
 Ile Asp Val Pro Leu Asp Phe Val Ala Arg Asp Val Ile Glu Asp Lys
 180 185 190
 Ser Gln Phe Ala Pro Ser Glu Ile Ser Ile Ser Gly Ser Tyr Pro Glu
 195 200 205
 Val Gln Asp Glu Leu Gly Ala Leu Tyr Asp Lys Tyr Arg Val Gly Tyr
 210 215 220
 Ala Thr Ala Asp Ala Ile Ile Ser Val Gln Lys Val Val Ser Arg Leu
 225 230 235 240
 Gly Cys Asp Asn Leu Asp Glu Ile Thr Arg Glu Asp Met Ala Leu Glu
 245 250 255
 Ala Leu Arg Glu Ile Glu Lys Leu Thr Arg Val Lys Lys Met Gln Glu
 260 265 270

Glu Ala Ala Arg Pro Phe
 275

<210> 23
 <211> 519
 <212> DNA
 <213> Glycine max

<400> 23
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 gggagaagac caccattcag tacatgtcgt ttgggtgtgt ctcggaacc gcagagcctt 180
 cgggtttttg tttcgccaat gatgatgcgg cgcagaacaa ccgctttgga ggtttcctct 240
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 gaagagctga ttctaaagaa tagatcacia gagaccagc catatttaaa tggacgctgt 360
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 gtgcttggtt attcattttg tgatagtgat gcattggttg aggacgacgt tgggtgaaac 480
 tctgtagccg atatatttga gcaacatggt gagactttc 519

<210> 24
 <211> 153
 <212> PRT
 <213> Glycine max

<400> 24
 Met Asp Val Lys Ala Ala Gln Arg Leu Gln Leu Ser Ala Val Val Gln
 1 5 10 15
 Pro Glu Arg Phe Gly Arg Arg Pro Pro Phe Ser Thr Cys Arg Leu Gly
 20 25 30
 Val Ser Arg Glu Pro Gln Ser Leu Arg Val Phe Val Ser Pro Met Met
 35 40 45
 Met Arg Arg Arg Thr Thr Ala Leu Glu Val Ser Ser Ser Tyr Asp Asn
 50 55 60

Ile Ser Ala Ser Ile Leu Glu Ser Gly Ser Val His Ala Pro Leu Asp
65 70 75 80

Glu Glu Leu Ile Leu Lys Asn Arg Ser Gln Glu Thr Gln Pro Tyr Leu
85 90 95

Asn Gly Arg Cys Ile Tyr Leu Val Gly Met Met Gly Ser Gly Lys Thr
100 105 110

Thr Val Gly Lys Ile Met Ser Gln Val Leu Gly Tyr Ser Phe Cys Asp
115 120 125

Ser Asp Ala Leu Val Glu Asp Asp Val Gly Gly Asn Ser Val Ala Asp
130 135 140

Ile Phe Glu Gln His Gly Glu Thr Phe
145 150

<210> 25
<211> 1323
<212> DNA
<213> Triticum aestivum

<400> 25
gcacgaggcc aaacgacgga agccgcaggg attccccccg gcgacagtgc cggcgggtgag 60
gctcgaccag aatccggcgc ggcggccgct ggtcctgcgc accgacgcgg ggagccggag 120
caccgatccc atccgtggcg ccagcctcaa ggccctgtgc tgccacaaat cggcaggtac 180
tgagaaagcc cactattctg ctgatgaggc tctcgtacta aagcaaaaag cagaggacgt 240
gctcccttac ctgaatgacc gctgtgttta tctagttaga atgatgggtt ccggcaaaac 300
tacagttggg aagataatag ctgaagtact aggctattca ttctttgaca gtgataagct 360
ggttgagcag tctgttggca taccgtcggg ggctgagatt tttcagggtc acagtgaagc 420
attcttcaga gataacgaga gtgaggtact aagggatttg tcgtcaatgc accgattaat 480
tgttgcaaca ggaggtgggtg cgggtgatacg accaatcaat tggagttata tgaagaaagg 540
actcactatt tgggttagatg ttccattgga cgcccttgca agaaggattg ctgcggttgg 600
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caaacttaca gcaactttttg aacaaagaat ggattcatat gctaattgctg atgcccgagt 720
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tgccatcgct attgagggcat tgctaaagat ggagagcttt cttactgaga aggccatggg 840
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ttgtcttgtc tttatcttgc tgcgatttga tatatgggat ttgggagtaa atagctatat 1080
catcgttaag tgatatccct tgtacatttt gacacaacca taatttacat caacatacta 1140
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cttataacct cctatcagat tctactgtat cccccggggg gggcccggtc tccaactctc 1260
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ggg 1323

<210> 26
<211> 282
<212> PRT
<213> Triticum aestivum

<400> 26
His Glu Ala Lys Arg Arg Lys Pro Gln Gly Phe Pro Pro Ala Thr Val
1 5 10 15

Pro Ala Val Arg Leu Asp Gln Asn Pro Ala Arg Arg Pro Leu Val Leu
20 25 30


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cagagataat gagagtagtg tcttgagggg tttgtcctca atgcggcgat tagttgttgc 420
tactggaggt ggtgctgtta tccgaccagt taactggaaa aatatgaaga agggcctatc 480
tgtttggttg gatgtgccct tggaaagctct tgcaaggcgt attgctaaag tggggactgc 540
ctcgcgtcct cttctagatc aaccatccgg tgatccatac acaatggcct tttcgaaaact 600
cagcatgctc gcggagcaaa ggggcgatgc ttatgcaa atgctgatgtca gagtttctct 660
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<210> 28
<211> 273
<212> PRT
<213> Triticum aestivum

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<400> 28
His Glu Val Ser Leu Arg Val Ser Asp Leu Val Gly Ser Pro Ala Ala
 1             5             10             15

Val Arg Ala Arg Gly Ala Lys Pro Val Val Pro Leu Arg Ala Lys Lys
          20             25             30

Ser Ser Gly Gly Gly His Glu Asn Leu His Asn Ser Val Asp Asp Ala
          35             40             45

Leu Leu Leu Lys Arg Lys Ser Glu Glu Val Leu Phe Gln Leu Asn Gly
 50             55             60

Arg Cys Ile Tyr Leu Val Gly Met Met Gly Ser Gly Lys Ser Thr Val
 65             70             75             80

Gly Lys Ile Leu Ala Glu Val Leu Gly Tyr Ser Phe Phe Asp Ser Asp
          85             90             95

Lys Leu Val Glu Gln Ala Val Gly Met Pro Ser Val Ala Gln Ile Phe
          100            105            110

Lys Val His Ser Glu Ala Phe Phe Arg Asp Asn Glu Ser Ser Val Leu
          115            120            125

Arg Asp Leu Ser Ser Met Arg Arg Leu Val Val Ala Thr Gly Gly Gly
          130            135            140

Ala Val Ile Arg Pro Val Asn Trp Lys Asn Met Lys Lys Gly Leu Ser
          145            150            155            160

Val Trp Leu Asp Val Pro Leu Glu Ala Leu Ala Arg Arg Ile Ala Lys
          165            170            175

Val Gly Thr Ala Ser Arg Pro Leu Leu Asp Gln Pro Ser Gly Asp Pro
          180            185            190

Tyr Thr Met Ala Phe Ser Lys Leu Ser Met Leu Ala Glu Gln Arg Gly
          195            200            205

Asp Ala Tyr Ala Asn Ala Asp Val Arg Val Ser Leu Glu Glu Ile Ala
          210            215            220

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Ser	Lys	Leu	Gly	His	Asp	Asp	Val	Ser	Lys	Leu	Thr	Pro	Ile	Asp	Ile
225					230					235					240
Ala	Leu	Glu	Ser	Leu	His	Lys	Ile	Glu	Ser	Phe	Val	Val	Glu	Asp	Thr
				245					250					255	
Ala	Val	Ala	Asp	Ser	Gln	Thr	Glu	Ser	Gln	Ser	Gln	Arg	Met	His	Thr
			260					265					270		
Leu															